

SEQUENCE LISTING

#4

COPY



(1) GENERAL INFORMATION:

- (i) APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelein, Robert A.
- (ii) TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 07-AUG-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/044,165
 - (B) FILING DATE: 21-APR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/055,111
 - (B) FILING DATE: 06-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/062,866
 - (B) FILING DATE: 20-APR-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/097,976
 - (B) FILING DATE: 16-JUN-1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0725K2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-852-9196
 - (B) TELEFAX: 650-496-1200

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG ATG GTT CTG AGT GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC
48
Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
1      5      10      15

TTG AAG GTA CTG TAT CTG CAC AAT AAC CAG CTG CTG GCT GGA GGA CTG
96
Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
20      25      30

CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT GTC CCA AAT
144
His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
35      40      45

CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA
192
Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
50      55      60

GGA AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA
240
Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
65      70      75      80

CTT GAG CCA GTG AAC ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA
288
Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
85      90      95

AAG AGC TTC ACC TTC TAC CGG CGG GAT ATG GGT CTT ACC TCC AGC TTC
336
Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
100      105      110

GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA CCG GAA GCT
384
Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
```

115 120 125

GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT
432

Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
130 135 140

GCT CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TA
470

Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
1 5 10 15

Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
20 25 30

His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
35 40 45

Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
50 55 60

Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
65 70 75 80

Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
85 90 95

Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
100 105 110

Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
115 120 125

Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
130 135 140

Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TTC CAG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA
48
Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val
 1           5           10           15

AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT
96
Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe
      20           25           30

GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG
144
Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly
      35           40           45

AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT
192
Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr
      50           55           60

GAC TTC GAG ATG ATT GTG GTA CAT TAA
219
Asp Phe Glu Met Ile Val Val His
65           70
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val
 1           5           10           15

Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe
      20           25           30

Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly
```

35

40

45

Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr
 50 55 60

Asp Phe Glu Met Ile Val Val His
 65 70

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 809 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 90..569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA CGAGTGTAGT GTGCAGACAC ATTCCTTATT CAATCAGGGT CAATCTGCAG
 60

ATTGGCAGCT CAGGAACAAC ATCACCATA ATG AAT AAG GAG AAA GAA CTA AGA
 113

Met Asn Lys Glu Lys Glu Leu Arg
 1 5

GCA GCA TCA CCT TCG CTT AGA CAT GTT CAG GAT CTT AGT AGT CGT GTG
 161
 Ala Ala Ser Pro Ser Leu Arg His Val Gln Asp Leu Ser Ser Arg Val
 10 15 20

TGG ATC CTG CAG AAC AAT ATC CTC ACT GCA GTC CCA AGG AAA GAG CAA
 209
 Trp Ile Leu Gln Asn Asn Ile Leu Thr Ala Val Pro Arg Lys Glu Gln
 25 30 35 40

ACA GTT CCA GTC ACT ATT ACC TTG CTC CCA TGC CAA TAT CTG GAC ACT
 257
 Thr Val Pro Val Thr Ile Thr Leu Leu Pro Cys Gln Tyr Leu Asp Thr
 45 50 55

CTT GAG ACG AAC AGG GGG GAT CCC ACG TAC ATG GGA GTG CAA AGG CCG
 305
 Leu Glu Thr Asn Arg Gly Asp Pro Thr Tyr Met Gly Val Gln Arg Pro
 60 65 70

ATG AGC TGC CTG TTC TGC ACA AAG GAT GGG GAG CAG CCT GTG CTA CAG
 353
 Met Ser Cys Leu Phe Cys Thr Lys Asp Gly Glu Gln Pro Val Leu Gln
 75 80 85

Leu Pro Cys Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro
 50 55 60
 Thr Tyr Met Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys
 65 70 75 80
 Asp Gly Glu Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu
 85 90 95
 Met Tyr Asn Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys
 100 105 110
 Lys Ser Gly Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp
 115 120 125
 Phe Ile Ala Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln
 130 135 140
 Glu Leu Gly Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
 1 5 10 15
 Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser
 20 25 30
 Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe
 35 40 45
 Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn
 50 55 60
 Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala
 65 70 75 80
 Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys
 85 90 95
 Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp
 100 105 110

Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser
 115 120 125
 Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp
 130 135 140
 Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn
 145 150 155 160
 Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp
 165 170 175
 Glu

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
 1 5 10 15
 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
 20 25 30
 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
 35 40 45
 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
 50 55 60
 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
 65 70 75 80
 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
 85 90 95
 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys
 100 105 110
 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
 115 120 125
 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
 130 135 140

His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
 145 150 155 160
 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
 165 170 175
 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
 180 185 190
 Asp

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
 1 5 10 15
 Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu
 20 25 30
 Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg
 35 40 45
 Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe
 50 55 60
 Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg
 65 70 75 80
 Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val
 85 90 95
 Thr Leu Ser Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn
 100 105 110
 Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp
 115 120 125
 Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn
 130 135 140
 Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys
 145 150 155 160
 Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu

165

170

175

Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
 180 185 190

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Glu Val Pro Lys Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser
 1 5 10 15

Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met
 20 25 30

Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile
 35 40 45

Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala
 50 55 60

Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro
 65 70 75 80

Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe
 85 90 95

Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala
 100 105 110

Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp
 115 120 125

Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala
 130 135 140

Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met
 145 150 155 160

Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu
 165 170 175

Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp
 180 185 190

Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys

195	200	205
Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn		
210	215	220
Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr		
225	230	235
Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly		
245	250	255
Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser		
260	265	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Lys	Val	Pro	Asp	Met	Phe	Glu	Asp	Leu	Lys	Asn	Cys	Tyr	Ser
1			5					10						15	
Glu	Asn	Glu	Glu	Asp	Ser	Ser	Ser	Ile	Asp	His	Leu	Ser	Leu	Asn	Gln
	20							25					30		
Lys	Ser	Phe	Tyr	His	Val	Ser	Tyr	Gly	Pro	Leu	His	Glu	Gly	Cys	Met
	35						40					45			
Asp	Gln	Ser	Val	Ser	Leu	Ser	Ile	Ser	Glu	Thr	Ser	Lys	Thr	Ser	Lys
	50					55					60				
Leu	Thr	Phe	Lys	Glu	Ser	Met	Val	Val	Val	Ala	Thr	Asn	Gly	Lys	Val
65					70					75					80
Leu	Lys	Lys	Arg	Arg	Leu	Ser	Leu	Ser	Gln	Ser	Ile	Thr	Asp	Asp	Asp
			85						90					95	
Leu	Glu	Ala	Ile	Ala	Asn	Asp	Ser	Glu	Glu	Glu	Ile	Ile	Lys	Pro	Arg
			100					105					110		
Ser	Ala	Pro	Phe	Ser	Phe	Leu	Ser	Asn	Val	Lys	Tyr	Asn	Phe	Met	Arg
	115						120					125			
Ile	Ile	Lys	Tyr	Glu	Phe	Ile	Leu	Asn	Asp	Ala	Leu	Asn	Gln	Ser	Ile
	130					135					140				
Ile	Arg	Ala	Asn	Asp	Gln	Tyr	Leu	Thr	Ala	Ala	Ala	Leu	His	Asn	Leu
145					150					155					160

Asp	Glu	Ala	Val	Lys	Phe	Asp	Met	Gly	Ala	Tyr	Lys	Ser	Ser	Lys	Asp
				165					170					175	
Asp	Ala	Lys	Ile	Thr	Val	Ile	Leu	Arg	Ile	Ser	Lys	Thr	Gln	Leu	Tyr
			180					185					190		
Val	Thr	Ala	Gln	Asp	Glu	Asp	Gln	Pro	Val	Leu	Leu	Lys	Glu	Met	Pro
			195				200					205			
Glu	Ile	Pro	Lys	Thr	Ile	Thr	Gly	Ser	Glu	Thr	Asn	Leu	Leu	Phe	Phe
	210					215					220				
Trp	Glu	Thr	His	Gly	Thr	Lys	Asn	Tyr	Phe	Thr	Ser	Val	Ala	His	Pro
225					230					235					240
Asn	Leu	Phe	Ile	Ala	Thr	Lys	Gln	Asp	Tyr	Trp	Val	Cys	Leu	Ala	Gly
				245					250					255	
Gly	Pro	Pro	Ser	Ile	Thr	Asp	Phe	Gln	Ile	Leu	Glu	Asn	Gln	Ala	
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..504

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 144
- (D) OTHER INFORMATION: /note= "nucleotide 144 designated

G, may be G or T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 451
- (D) OTHER INFORMATION: /note= "nucleotide 451 designated

C, may be C or T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 469
- (D) OTHER INFORMATION: /note= "nucleotide 469 designated

C, may be A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC GTC TAT
 48
 Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1 5 10 15
 CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG AAT CAG
 96
 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
 20 25 30
 CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA CGA AGG
 144
 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg
 35 40 45
 ACC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG TAT CCA
 192
 Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
 50 55 60
 GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA ATC CAG
 240
 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
 65 70 75 80
 AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG CCC ACA
 288
 Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
 85 90 95
 TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA CCC GAG
 336
 Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
 100 105 110
 CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG ACC TCC
 384
 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
 115 120 125
 ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC TCC AAG
 432
 Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
 130 135 140
 GGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT TGG CAG TCA TAC AAC
 480
 Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn
 145 150 155 160
 ACT GCC TTT GAA TTA AAT ATT AAT G
 505
 Thr Ala Phe Glu Leu Asn Ile Asn
 165

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1           5           10           15
Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
          20           25           30
Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Arg
          35           40           45
Thr Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
          50           55           60
Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
          65           70           75           80
Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
          85           90           95
Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
          100          105          110
Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
          115          120          125
Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
          130          135          140
Gly Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Trp Gln Ser Tyr Asn
          145          150          155          160
Thr Ala Phe Glu Leu Asn Ile Asn
          165

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 67..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCACGATTCA GTCCCCTGGA CTGTAGATAA AGACCCTTTC TTGCCAGGTG CTGAGACAAC
60

CACACT ATG AGA GGC ACT CCA GGA GAC GCT GAT GGT GGA GGA AGG GCC
108

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala
1 5 10

GTC TAT CAA TCA ATG TGT AAA CCT ATT ACT GGG ACT ATT AAT GAT TTG
156

Val Tyr Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu
15 20 25 30

AAT CAG CAA GTG TGG ACC CTT CAG GGT CAG AAC CTT GTG GCA GTT CCA
204

Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro
35 40 45

CGA AGT GAC AGT GTG ACC CCA GTC ACT GTT GCT GTT ATC ACA TGC AAG
252

Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys
50 55 60

TAT CCA GAG GCT CTT GAG CAA GGC AGA GGG GAT CCC ATT TAT TTG GGA
300

Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly
65 70 75

ATC CAG AAT CCA GAA ATG TGT TTG TAT TGT GAG AAG GTT GGA GAA CAG
348

Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln
80 85 90

CCC ACA TTG CAG CTA AAA GAG CAG AAG ATC ATG GAT CTG TAT GGC CAA
396

Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
95 100 105 110

CCC GAG CCC GTG AAA CCC TTC CTT TTC TAC CGT GCC AAG ACT GGT AGG
444

Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg
115 120 125

ACC TCC ACC CTT GAG TCT GTG GCC TTC CCG GAC TGG TTC ATT GCC TCC
492

Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser
130 135 140

TCC AAG AGA GAC CAG CCC ATC ATT CTG ACT TCA GAA CTT GGG AAG TCA
540

Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser
145 150 155

TAC AAC ACT GCC TTT GAA TTA AAT ATA AAT GAC TGA ACT CAGC CTAGAGGTGG
593

Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp

160

165

CAGCTTGGTC TTTGTCTTAA AGTTTCTGGT TCCCAATGTG TTTTCGTCTA CATTTTCTTA
653

GTGTCATTTT CACGCTGGTG CTGAGACAGG GGCAAGGCTG CTGTTATCAT CTCATTTTAT
713

AATGAAGAAG AAGCAATTAC TTCATAGCAA CTGAAGAACA GGATGTGGCC TCAGAAGCAG
773

GAGAGCTGGG TGGTATAAGG CTGTCCTCTC AAGCTGGTGC TGTGTAGGCC ACAAGGCATC
833

TGCATGAGTG ACTTTAAGAC TCAAAGACCA AACACTGAGC TTTCTTCTAG GGGTGGGTAT
893

GAAGATGCTT CAGAGCTCAT GCGCGTTACC CACGATGGCA TGACTIONCAC AGAGCTGATC
953

TCTGTTTCTG TTTTGCTTTA TTCCCTCTTG GGATGATATC ATCCAGTCTT TATATGTTGC
1013

CAATATACCT CATTGTGTGT AATAGAACCT TCTTAGCATT AAGACCTTGT AAACAAAAAT
1073

AATTCCTGTG TTAAGTTAAA TCATTTTGT CCTAATTGTA ATGTGTAATC TTAAAGTTAA
1133

ATAAACTTGT TGTATTTATA TAATAATAAA GCTAAACTG ATATAAAAAA AAAAAAAAAA
1193

AA
1195

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Arg	Gly	Thr	Pro	Gly	Asp	Ala	Asp	Gly	Gly	Gly	Arg	Ala	Val	Tyr
1				5					10					15	

Gln	Ser	Met	Cys	Lys	Pro	Ile	Thr	Gly	Thr	Ile	Asn	Asp	Leu	Asn	Gln
			20					25					30		

Gln	Val	Trp	Thr	Leu	Gln	Gly	Gln	Asn	Leu	Val	Ala	Val	Pro	Arg	Ser
		35				40						45			

Asp	Ser	Val	Thr	Pro	Val	Thr	Val	Ala	Val	Ile	Thr	Cys	Lys	Tyr	Pro
		50				55					60				

Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
65 70 75 80

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
85 90 95

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
100 105 110

Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
115 120 125

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
130 135 140

Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
145 150 155 160

Thr Ala Phe Glu Leu Asn Ile Asn Asp
165